

77 ✓

526 Rec'd PCT/PTO 13 NOV 2000

SEQUENCE LISTING

<110> The University of Queensland
 National Institute of Biological Standards and Control

<120> Novel anti-fibrinolytic agents

<130> Textilininins

<140> PCT/AU99/OXXX
 <141> 1999-05-10

<150> AU PP3450
 <151> 1999-05-11

<160> 44

<170> PatentIn Ver. 2.0

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 Arg Val Arg Phe Pro Ser Phe Tyr Tyr Asn Pro Asp Glu Lys Lys Cys
 20 25 30
 cta gag ttt att tat ggt gga tgc gaa ggg aat gct aac aat ttt atc 144
 Leu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Ile
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Arg Val Arg Phe Pro Ser Phe Tyr Tyr Asn Pro Asp Glu Lys Lys Cys
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aga gtc aga ttc cca tcc ttc tac tac aac cca gat gaa caa aaa tgc 96
Arg Val Arg Phe Pro Ser Phe Tyr Tyr Asn Pro Asp Glu Gln Lys Cys
20 25 30
cta gag ttt att tat ggt gga tgc gaa ggg aat gct aac aat ttt atc 144
Leu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Ile
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acc aaa gag gaa tgc gaa agc acc tgt gct gcc tga 180
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 Asn Ala Lys Ile Pro Arg Phe Tyr Tyr Asn Pro Arg Gln His Gln Cys
 20 25 30
 ata gag ttt ctc tat ggt gga tgc gga ggg aat gct aac aat ttt aag 144
 Ile Glu Phe Leu Tyr Gly Gly Cys Gly Gly Asn Ala Asn Asn Phe Lys
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 acc att aag gaa tgc gaa agc acc tgt gct gca tga 180
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 <212> PRT
 <213> Pseudonaja textilis

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 Lys Gly Asn Val Pro Arg Phe Tyr Tyr Asn Ala Asp His His Gln Cys
 20 25 30
 cta aaa ttt att tat ggt gga tgt gga ggg aat gct aac aat ttt aag 144
 Leu Lys Phe Ile Tyr Gly Gly Cys Gly Gly Asn Ala Asn Asn Phe Lys
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 Lys Asp Arg Pro Lys Phe Cys Glu Leu Leu Pro Asp Thr Gly Ser Cys
 1 5 10 15
 gaa gac ttt acc gga gcc ttc cac tac agc aca cgt gat cgt gaa tgc 96
 Glu Asp Phe Thr Gly Ala Phe His Tyr Ser Thr Arg Asp Arg Glu Cys
 20 25 30
 ata gag ttt att tat ggt gga tgc gga ggg aat gct aac aat ttt atc 144
 Ile Glu Phe Ile Tyr Gly Gly Cys Gly Gly Asn Ala Asn Asn Phe Ile
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 Thr Lys Glu Glu Cys Glu Ser Thr Cys Ala Ala
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 gat gac ttt acc gga gcc ttc cac tac agc cca cgt gaa cat gaa tgc 96
 Asp Asp Phe Thr Gly Ala Phe His Tyr Ser Pro Arg Glu His Glu Cys
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Met Ser Ser Gly Gly Leu Leu Leu Leu Leu Gly Leu Leu Thr Leu Trp
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Glu Val Leu Thr Pro Val Ser Ser
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<210> 15
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-20 -15 -10

gag gtg ctg acc ccc gtc tcc agc aag gac cgt ccg gat ttc tgt gaa 96
Glu Val Leu Thr Pro Val Ser Ser Lys Asp Arg Pro Asp Phe Cys Glu
-5 -1 1 5

ctg cct gct gac acc gga cca tgt aga gtc aga ttc cca tcc ttc tac 144
Leu Pro Ala Asp Thr Gly Pro Cys Arg Val Arg Phe Pro Ser Phe Tyr
10 15 20

tac aac cca gat gaa aaa aag tgc cta gag ttt att tat ggt gga tgc 192
Tyr Asn Pro Asp Glu Lys Lys Cys Leu Glu Phe Ile Tyr Gly Gly Cys
25 30 35 40

gaa ggg aat gct aac aat ttt atc acc aaa gag gaa tgc gaa agc acc 240
Glu Gly Asn Ala Asn Asn Phe Ile Thr Lys Glu Glu Cys Glu Ser Thr
45 50 55

tgt gct gcc tga 252
Cys Ala Ala
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Glu Val Leu Thr Pro Val Ser Ser Lys Asp Arg Pro Asp Phe Cys Glu
20 25 30

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Leu Pro Ala Asp Thr Gly Pro Cys Arg Val Arg Phe Pro Ser Phe Tyr
 35 40 45

Tyr Asn Pro Asp Glu Lys Lys Cys Leu Glu Phe Ile Tyr Gly Gly Cys
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Cys Ala Ala

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gag gtg ctg acc ccc gtc tcc agc aag gac cgt cca gag ttg tgt gaa 96
 Glu Val Leu Thr Pro Val Ser Ser Lys Asp Arg Pro Glu Leu Cys Glu
 -5 -1 1 5

ctg cct cct gac acc gga cca tgt aga gtc aga ttc cca tcc ttc tac 144
 Leu Pro Pro Asp Thr Gly Pro Cys Arg Val Arg Phe Pro Ser Phe Tyr
 10 15 20

tac aac cca gat gaa caa aaa tgc cta gag ttt att tat ggt gga tgc 192
 Tyr Asn Pro Asp Glu Gln Lys Cys Leu Glu Phe Ile Tyr Gly Gly Cys
 25 30 35 40

gaa ggg aat gct aac aat ttt atc acc aaa gag gaa tgc gaa agc acc 240
 Glu Gly Asn Ala Asn Asn Phe Ile Thr Lys Glu Glu Cys Glu Ser Thr
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tgt gct gcc tga 252
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<210> 18

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<400> 18

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 Leu Pro Pro Asp Thr Gly Pro Cys Arg Val Arg Phe Pro Ser Phe Tyr
 35 40 45
 Tyr Asn Pro Asp Glu Gln Lys Cys Leu Glu Phe Ile Tyr Gly Gly Cys
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 gag gtg ctg acc ccc gtc tcc agc aag gac cgt cca aat ttc tgt aaa 96
 Glu Val Leu Thr Pro Val Ser Ser Lys Asp Arg Pro Asn Phe Cys Lys
 -5 -1 1 5
 ctg cct gct gaa acc gga cga tgt aat gcc aaa atc cca cgc ttc tac 144
 Leu Pro Ala Glu Thr Gly Arg Cys Asn Ala Lys Ile Pro Arg Phe Tyr
 10 15 20
 tac aac cca cgt caa cat caa tgc ata gag ttt ctc tat ggt gga tgc 192
 Tyr Asn Pro Arg Gln His Gln Cys Ile Glu Phe Leu Tyr Gly Gly Cys
 25 30 35 40
 gga ggg aat gct aac aat ttt aag acc att aag gaa tgc gaa agc acc 240
 Gly Gly Asn Ala Asn Asn Phe Lys Thr Ile Lys Glu Cys Glu Ser Thr
 45 50 55
 tgt gct gca tga 252

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Cys Ala Ala

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			20					25					30		

Leu	Pro	Ala	Glu	Thr	Gly	Arg	Cys	Asn	Ala	Lys	Ile	Pro	Arg	Phe	Tyr
		35					40					45			

Tyr	Asn	Pro	Arg	Gln	His	Gln	Cys	Ile	Glu	Phe	Leu	Tyr	Gly	Gly	Cys
	50					55					60				

Gly	Gly	Asn	Ala	Asn	Asn	Phe	Lys	Thr	Ile	Lys	Glu	Cys	Glu	Ser	Thr
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Cys Ala Ala

<210> 21

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Met	Ser	Ser	Gly	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Thr	Leu	Trp	
				-20					-15				-10			

gag	gtg	ctg	acc	ccc	gtc	tcc	agc	aag	gac	cat	cca	aaa	ttc	tgt	gaa	96
Glu	Val	Leu	Thr	Pro	Val	Ser	Ser	Lys	Asp	His	Pro	Lys	Phe	Cys	Glu	
			-5				-1	1				5				

ctc	cct	gct	gaa	acc	gga	tca	tgt	aaa	ggc	aac	gtc	cca	cgc	ttc	tac	144
Leu	Pro	Ala	Glu	Thr	Gly	Ser	Cys	Lys	Gly	Asn	Val	Pro	Arg	Phe	Tyr	
	10					15					20					

tac	aac	gca	gat	cat	cat	caa	tgc	cta	aaa	ttt	att	tat	ggt	gga	tgt	192
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Tyr Asn Ala Asp His His Gln Cys Leu Lys Phe Ile Tyr Gly Gly Cys
 25 30 35 40
 gga ggg aat gct aac aat ttt aag acc ata gag gaa ggc aaa agc acc 240
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 tgt gct gcc tga 252
 Cys Ala Ala
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 35 40 45
 Tyr Asn Ala Asp His His Gln Cys Leu Lys Phe Ile Tyr Gly Gly Cys
 50 55 60
 Gly Gly Asn Ala Asn Asn Phe Lys Thr Ile Glu Glu Gly Lys Ser Thr
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 Cys Ala Ala

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 gag gtg ctg acc ccc gtc tcc agc aag gac cgt cca aaa ttc tgt gaa 96

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Glu Val Leu Thr Pro Val Ser Ser Lys Asp Arg Pro Lys Phe Cys Glu
 -5 -1 1 5
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 Leu Leu Pro Asp Thr Gly Ser Cys Glu Asp Phe Thr Gly Ala Phe His
 10 15 20
 tac agc aca cgt gat cgt gaa tgc ata gag ttt att tat ggt gga tgc 192
 Tyr Ser Thr Arg Asp Arg Glu Cys Ile Glu Phe Ile Tyr Gly Gly Cys
 25 30 35 40
 gga ggg aat gct aac aat ttt atc acc aaa gag gaa tgc gaa agc acc 240
 Gly Gly Asn Ala Asn Asn Phe Ile Thr Lys Glu Glu Cys Glu Ser Thr
 45 50 55
 tgt gct gcc tga 252
 Cys Ala Ala
 60

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 20 25 30
 Leu Leu Pro Asp Thr Gly Ser Cys Glu Asp Phe Thr Gly Ala Phe His
 35 40 45
 Tyr Ser Thr Arg Asp Arg Glu Cys Ile Glu Phe Ile Tyr Gly Gly Cys
 50 55 60
 Gly Gly Asn Ala Asn Asn Phe Ile Thr Lys Glu Glu Cys Glu Ser Thr
 65 70 75 80
 Cys Ala Ala

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Met	Ser	Ser	Gly	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Thr	Leu	Trp	
			-20						-15				-10			

gag	gtg	ctg	acc	ccc	gtc	tcc	agc	aag	gac	cgt	cca	aag	ttc	tgt	gaa	96
Glu	Val	Leu	Thr	Pro	Val	Ser	Ser	Lys	Asp	Arg	Pro	Lys	Phe	Cys	Glu	
			-5				-1	1				5				

ctg	cct	gct	gac	atc	gga	cca	tgg	gat	gac	ttt	acc	gga	gcc	ttc	cac	144
Leu	Pro	Ala	Asp	Ile	Gly	Pro	Trp	Asp	Asp	Phe	Thr	Gly	Ala	Phe	His	
	10					15					20					

tac	agc	cca	cgt	gaa	cat	gaa	tgc	ata	gag	ttt	att	tat	ggt	gga	tgc	192
Tyr	Ser	Pro	Arg	Glu	His	Glu	Cys	Ile	Glu	Phe	Ile	Tyr	Gly	Gly	Cys	
	25				30				35						40	

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Lys	Gly	Asn	Ala	Asn	Asn	Phe	Asn	Thr	Gln	Glu	Gln	Cys	Glu	Ser	Thr	
			45						50					55		

tgt	gct	gcc	tga													252
Cys	Ala	Ala														
			60													

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<212> PRT

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Met	Ser	Ser	Gly	Gly	Leu	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Thr	Leu	Trp	
	1			5					10					15		

Glu	Val	Leu	Thr	Pro	Val	Ser	Ser	Lys	Asp	Arg	Pro	Lys	Phe	Cys	Glu	
			20					25					30			

Leu	Pro	Ala	Asp	Ile	Gly	Pro	Trp	Asp	Asp	Phe	Thr	Gly	Ala	Phe	His	
		35					40					45				

Tyr	Ser	Pro	Arg	Glu	His	Glu	Cys	Ile	Glu	Phe	Ile	Tyr	Gly	Gly	Cys	
	50					55					60					

Lys	Gly	Asn	Ala	Asn	Asn	Phe	Asn	Thr	Gln	Glu	Gln	Cys	Glu	Ser	Thr	
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Cys Ala Ala

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gtrctytcrt gytctytcy	18
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<223> Description of Artificial Sequence:gene-specific forward primer for Txln1	
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<223> Description of Artificial Sequence:RACE-ready long
universal reverse primer

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<223> Description of Artificial Sequence:RACE-ready
short universal reverse primer

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<223> Description of Artificial Sequence:RACE-ready
nested universal reverse primer

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<223> Description of Artificial Sequence:Txln1-gene
specific forward primer

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<223> Description of Artificial Sequence:Txln1
gene-specific reverse primer

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xvi

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27

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<223> Description of Artificial Sequence:Txln-active
peptide sequence forward primer

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forward primer for txln2

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:gene-specific
forward primer for Txln3

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 Thr Leu Trp Glu Val Leu Thr Pro Val Ser Ser Lys Asp Arg Pro Glu
 -10 -5 -1 1 5

ttg tgt gaa ctg cct cct gac acc gga cca tgt aga gtc aga tcc cca 146
 Leu Cys Glu Leu Pro Pro Asp Thr Gly Pro Cys Arg Val Arg Ser Pro
 10 15 20

tcc ttc tac tac aac cca gat gaa caa aaa tgc cta gag ttt att 191
 Ser Phe Tyr Tyr Asn Pro Asp Glu Gln Lys Cys Leu Glu Phe Ile
 25 30 35

tatggtggat gcgaaggga tgctaaccaa ttttatcacc aaagaggaat gcgaaagcac 251

